## What is Claimed is:

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1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on at least one copy of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	10	PS	PS	Har	olotype	e Numi	ber(c)	(Part 1	)				
		No.(a)	Position(b)	1	2	3	4	5	6 -	7	8	9	10
Šæri:		1	504	G	G	G	G	G	G	G	G	G	G
		2	717	С	C	C	C	C	C	C	C	C	C
		3.	744	G	G	G	G	G	G	G	G	G	G
	15	4	778	C	C	C	C	C	С	C	T	T	T
- jac ins		5	1009	C	C	G	G	G	G	G	C	C	C
ā		6	1045	C	C	T	T	T	T	T	C	C	C
7,1		7	1122	G	G	Α	G	G	G	G	G	G	G
engles Jaco		8	1218	C	C	C	$\mathbf{C}$	C	C	С	A	Α	C
9	20	9	2014	C	C	C	C	C	C	T	C	С	C
		10	2177	T	T	T	T	T	T	C	T	T	T
		11	5906	C	T	T	C	$\mathbf{T}$	T	T	C	T	C
		12	6010	C	C	C	C	C	T	T	C	C	C
127		13	8110	G	G	G	G	G	G	G	G	G	G
	25	14	8333	C	C	C	C	C	C	T	C	C	C
T.		15	8354	Α	Α	Α	A	A	A	Α	G	A	Α
		16	8402	A	Α	Α	A	A	A	G	Α	Α	Α
		17	8459	Α	Α	Α	Α	A	A	A	Α	A	A
		18	10203	G	G	G	G	G	G	G	G	G	G
	30	19	10512	T	T	C	T	T	T	T	T	T	T

		PS	PS	Har	olotype	Num	ber(c)	(Part 2	)				
		No.(a)	Position(b)	11	12	13	14	15	16	17	18	19	20
		1	504	G	G	G	G	G	G	G	G	G	G
	5	2	717	Č	Č	C	C	С	C	C	C	C	C
	,	3	744	Ğ	Ğ	$_{ m j}$ $\ddot{ m G}$	G	G	G	G	G	G	T
		4	778	Ť	Ť	T	T	T	T	T	T	T	T
		5	1009	Ĉ	Ĉ	Ğ	G	G	G	G	G	G	G
		6	1045	Č	Č	Č	Č	C	C	C'	C	C	C
	10	. 7	1122	Ğ	Ğ	Ğ	Ğ	G	G	G	G	G	G
	10	8	1218	Č	Č	Ā	Ā	A	C	C	С	C	C
		9	2014	Č	Ť	C	C	C	C	C	C	C	C
		10	2177	T	Ĉ	T	T	T	T	T	T	T	T
		11	5906	T	Ť	C	T	T	C	T	T	T	T
	15	12	6010	Ĉ	Ĉ	C	C	C	C	C	C	C	C
Jania	13	13	8110	Ğ	Ğ	Ā	G	G	G	A	G	G	G
		14	8333	Č	Č	C	C	C	C	C	C	C	C
		15	8354	A	Ā	Ā	A	A	Α	A	Α	Α	A
3213 3213		16	8402	A	G	A	Α	A	Α	Α	Α	A	Α
2022	20	17	8459	A	Č	A	Α	A	Α	Α	Α	Α	Α
	20	18	10203	A	Ğ	G	G	G	G	G	G	G	G
74.1		19	10512	T	Ť	Ċ	C	T	T	T	C	T	T
The state and the state		10	10312	-	_	_							
89		PS	PS	Ha	plotyp	e Nun	nber(c)	(Part	3)				
	25	No.(a)	Position(b)	21	22		` `	`					
		1	504	G	T								
		2	717	T	C								
		3	744	G	G								
2000		4	778	C	T								
	30	5	1009	С	G								
		6	1045	C	C								
		7	1122	G	G								
		8	1218	C	C								
		9	2014	C	C								
	35	10	2177	T	T								
		11	5906	C	T								
		12	6010	C	C								
		13	8110	G	Α								
		14	8333	C	C						-		~
	40	15	8354	Α	Α							•	
		16	8402	Α	Α								
		17	8459	A	Α								
		18	10203	G	G								
		19	10512	T	C								
	45												

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5' to 3' in each column.

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on both copies of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

	10	PS	PS	Hap	olotype I	Pair(c) (F	art 1)				
Company Company		No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
pres.		1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
1		3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
The state of the s	15	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
200		5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
4		6 .	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
The state of the s		7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
2	20	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	· C/C	C/C
		10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
		11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
		. 12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
		13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
C T	25	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
14		15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
		16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
	•	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
•		18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	30	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

		PS	PS	Hap	lotype P	air(c) (P	art 2)				
		No.(a)	Position(b)	,10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
		1	- 504	G/G							
		2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
•	5	3	744	G/G							
		4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
		5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
		6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
		7	1122	G/G							
	10	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C C/C
		9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C T/T	T/T
		10	2177	T/T	T/T	T/T	T/C	T/T	T/T T/T	T/T	C/T
		11	5906	C/T	T/T	T/C	T/T	C/C C/C	C/C	C/T	C/T
		12	6010	C/C	C/C	C/C	C/C G/G	G/G	G/G	G/G	G/G
1 :	15	13	8110	G/G	G/G	G/A C/C	C/C	C/C	C/C	C/C	C/C
		14	8333	C/C	C/C	A/A	A/A	A/A	A/A	A/A	A/A
, intel		15	8354	A/A	A/A A/A	A/A A/A	A/G	A/A	A/A	A/A	A/A
insi pu		16	8402	A/A A/A	A/A A/A	A/A A/A	A/C	A/A	A/A	A/A	A/A
1111	20	17	8459	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000	20	18 19	10203 10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
		19	10312	1/0	1/0	1,0	1/1	2, 2			
======================================											
3		PS	PS	Hap	olotype I	Pair(c) (	Part 3)				
	25	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
h	•	1	504	G/G							
		2	717	C/C							
		3	744	G/G	G/Ģ	G/G	G/G	G/G	G/T	G/G	G/G
		4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T G/G
Ti.	30	5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G C/T	C/C
		6	1045	C/C	C/T	C/T	C/C	C/T G/A	C/C G/G	G/G	G/G
		7	1122	G/G	G/G	G/A	G/G C/A	A/C	- C/C	C/C	C/C
-		8	1218	C/C	C/C	C/C C/C	C/A C/C	C/C	C/C	C/T	C/C
	2.5	9	2014	C/C T/T	C/C T/T	T/T	T/T	T/T	T/T	T/C	T/T
	35	10	2177	1/1 C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
		. 11	5906 6010	C/T	C/C	C/C	C/C	C/C	C/C	C/T	C/C
		12 13	8110	G/G							
		13	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	40	15	8354	A/A	A/A	A/A	A/A	A/A		A/A	A/A
	40	16	8402	A/A	A/A	A/A	A/A	A/A		A/G	A/A
		17	8459	A/A	A/A	A/A	A/A	A/A		A/A	A/A
		18	10203	G/G	G/G	G/G	G/G	G/G		G/G	G/G
		19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C
	45							~			

		PS	PS	Hap	lotype P	air(c) (P	art 4)				
		No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
		1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	5	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
		5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
		6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
		7	1122	G/G	G/G	G/G	G/G		G/G	G/G	G/G
	10	. 8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
		9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
		10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
<u> </u>		11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
		12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C G/G
	15	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	C/C
	1	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	A/A
7227		15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A A/A
	٠.	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A A/A
=======================================		17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	G/G
	20	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G T/T	C/T
		19	10512	C/T	T/T	T/T	T/T	T/T	T/T	1/1	C/ I
792											
222		DO:	DC	LI	alatema I	Dair(a) (	Part 5)				
		PS	PS Position(b)		olotype l	Pair(c) (	Part 5)				
₹ .	25	No.(a)	Position(b)	3/14	olotype I	Pair(c) (l	Part 5)				
=	25	No.(a) 1	Position(b) 504	3/14 G/G	olotype I	Pair(c) (I	Part 5)				
	25	No.(a) 1 2	Position(b) 504 717	3/14 G/G C/C	olotype l	Pair(c) (I	Part 5)				
	25	No.(a) 1 2 3	Position(b) 504 717 744	3/14 G/G C/C G/G	olotype l	Pair(c) (I	Part 5)				
	25	No.(a) 1 2 3 4	Position(b) 504 717 744 778	3/14 G/G C/C G/G C/T	olotype l	Pair(c) (I	Part 5)				
		No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	3/14 G/G C/C G/G C/T G/G	olotype l	Pair(c) (I	Part 5)				
	25	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	3/14 G/G G/G C/C G/G C/T G/G T/C	olotype l	Pair(c) (I	Part 5)				
		No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	3/14 G/G C/C G/G C/T G/G	olotype l	Pair(c) (I	Part 5)				
		No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	olotype l	Pair(c) (I	Part 5)				
		No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122	3/14 G/G C/C G/G C/T G/G T/C A/G	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	olotype l	Pair(c) (I	Part 5)				
		No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A	olotype l	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	olotype I	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459 10203	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A A/A	olotype I	Pair(c) (I	Part 5)				
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	olotype I	Pair(c) (I	Part 5)				

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<sup>(</sup>a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1<sup>st</sup> haplotype/2<sup>nd</sup> haplotype; with alleles of each haplotype shown 5' to 3' as 1<sup>st</sup> polymorphism/2<sup>nd</sup> polymorphism in each column.

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- 3. A method for genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, comprising determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the one or more polymorphic sites (PS) have the position and alternative alleles shown in SEQ ID NO:1.
- 4. The method of claim 3, wherein the determining step comprises:
  - isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF11B gene, or a fragment thereof, that are present in the individual;
  - (b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;
  - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;
  - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
  - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
- 5. The method of claim 3, which comprises determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at each of PS1-PS19.
- 6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual which comprises determining, for one copy of the TNFRSF11B gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 7. The method of claim 6, further comprising determining the identity of the nucleotide at PS5, wherein the PS has the position and alternative alleles shown in SEQ ID NO:1.
- 8. The method of claim 6, wherein the determining step comprises:
  - (a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF11B gene, or a fragment thereof, that is present in the individual;
  - (b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;
  - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in

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the target region;

- (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
  - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
- 9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual comprising:
  - (a) identifying a TNFRSF11B genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;
  - (b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and
- (c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

	PS	PS	Нар	lotype P	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
15	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
10	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
20	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
25	11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
30	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

35	PS	PS	Hap	lotype P	air(c) (P	art 2)				
33	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
40	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
70	5	1009	C/G	G/G	G/G	G/C	Ċ/C	G/C	G/G	C/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	. 8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
45	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
,,,	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
50	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
00,	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
55	19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
	-				<b>.</b>	D (2)				
	PS	PS		olotype l			15/2	19/20	19/7	19/18
	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3 G/G	19/20 G/G	G/G	G/G
	1	504	G/G	G/G	G/G	G/G C/C	C/C	C/C	C/C	C/C
60	2	717	C/C	C/C	C/C	G/G	G/G	G/T	G/G	G/G
	3	744	G/G	G/G	G/G T/C	T/T	T/C	T/T	T/C	T/T
	4	778	C/C	T/C G/G	G/G	G/C	G/G	G/G	G/G	G/G
	5	1009	C/C C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
~ ~	6	1045	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
65	7	1122	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
	8	1218	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	9	2014 2177	T/T	T/T	T/T	T/T	T/T	T/T	T/C	T/T
	10	5906	C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
70	11 12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
70	13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	13	8333	C/C	C/C	C/C	C/C	· C/C	C/C	C/T	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
75	17	8459	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
13	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10203	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

80	PS No.(a)	PS Position(b) 504	22/17 T/G	lotype P 19/12 G/G	1/12 G/G	19/8 G/G	15/10 G/G	19/15 G/G	19/10 G/G	18/16 G/G
	2 3	717	C/C	C/C G/G	C/C G/G	C/C G/G	C/C	C/C G/G	C/C G/G	C/C G/G
	<i>3</i> 4	744 778	G/G T/T	T/T	C/T	T/T	G/G T/T	T/T	T/T	T/T
85	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
•	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
90	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
95	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
100	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T
100	DC	DC	Han	lotme P	air(c) (I	Part 5)				
100	PS No.(a)	PS Position(b)		lotype P	air(c) (I	Part 5)			^	
100	No.(a)	Position(b)	3/14	lotype P	air(c) (I	Part 5)			•	
100	No.(a)	Position(b) 504	3/14 G/G	lotype P	air(c) (I	Part 5)				
	No.(a) 1 2	Position(b) 504 717	3/14 G/G C/C	lotype P	air(c) (I	Part 5)			•	
105	No.(a)	Position(b) 504	3/14 G/G	lotype F	air(c) (I	Part 5)				
	No.(a) 1 2 3	Position(b) 504 717 744	3/14 G/G C/C G/G	lotype P	air(c) (I	Part 5)				
	No.(a) 1 2 3 4	Position(b) 504 717 744 778	3/14 G/G C/C G/G C/T	lotype P	'air(c) (I	art 5)				
	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	3/14 G/G C/C G/G C/T G/G T/C A/G	lotype P	'air(c) (I	art 5)				
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	air(c) (I	Part 5)				
105 110 115	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	air(c) (I	Part 5)				

- (a) PS = polymorphic site;
- (b) Position of PS in SEQ ID NO:1;
- (c) Haplotype pairs are represented as 1<sup>st</sup> haplotype/2<sup>nd</sup> haplotype; with alleles of each haplotype shown 5' to 3' as 1<sup>st</sup> polymorphism/2<sup>nd</sup> polymorphism in each column.
  - 10. The method of claim 9, wherein the identified genotype of the individual comprises the nucleotide pair at each of PS1-PS19, which have the position and alternative alleles shown in SEQ ID NO:1.
  - 11. A method for identifying an association between a trait and at least one haplotype or haplotype

pair of the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)

(TNFRSF11B) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-22 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	PS	PS	Hap	lotype	Numb	er(c) (	Part 1)	)			~	
	No.(a)	Position(b)	1	2	3	4	5	6	7	8	9	10
	1	504	G	G	G	G	G	G	G	G	G	G
15	2	717	C	C	C	C	C	C	C	C	C	C
10	3	744	G	G	G	G	G	G	G	G	G	G
	4	778	C	C	C	C	C	C	C	T	T	T
	5	1009	C	C	G	G	G	G	G	C	C	C
	6	1045	C	C	T	T	T	T	T	C	C	C
20	7	1122	G	G	Α	G	G	G	G	G	G	G
	8	1218	C	C	C	C	C	C	C	Α	Α	C
	9	2014	C	C	C	C	C	C	T	C	C	C
	10	2177	T	T	T	T	T	T	C	T	T	T
	11	5906	C	T	T	C	T	T	T	C	T	C
25	12	6010	C	C	C	C	C	T	T	C	C	C
	13	8110	G	G	G	G	G	G	G	G	G	G
	14	8333	C	C	$\mathbf{C}$	C	C	C	T	C	C	C
	15	8354	$\mathbf{A}$	Α	Α	Α	Α	Α	Α	G	Α	A
	16	8402	Α	Α	A	Α	Α	A	G	Α	Α	A
30	17	8459	Α	A	Α	A	Α	Α	Α	A	Α	A
	18	10203	G	G	G	G	G	G	G	G	G	G
	19	10512	T	T	C	T	T	T	T	T	T	T
	PS	PS	Ha	plotyp			(Part 2	2)	_		10	20
35		PS Position(b)	На 11	12	13	14	15	16	17	18	19	20
35.	PS No.(a)		11 G	12 G	13 G	14 G	15 G	16 G	G	G	G	G
35	No.(a)	Position(b)	11 G C	12 G C	13 G C	14 G C	15 G C	16 G C	G C	G C	G C	G C
35	No.(a) 1	Position(b) 504	11 G C G	12 G C G	13 G C G	14 G C G	15 G C G	16 G C G	G C G	G C G	G C G	G C T
35	No.(a) 1 2 3 4	Position(b) 504 717 744 778	II G C G T	12 G C G T	13 G C G T	14 G C G T	15 G C G T	16 G C G T	G C G T	G C G T	G C G T	G C T T
35 40	No.(a) 1 2 3	Position(b) 504 717 744 778 1009	G C G T C	G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G	G C G T G	G C G T G	G C T T G
	No.(a) 1 2 3 4	Position(b) 504 717 744 778 1009 1045	II G C G T C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G C	G C G T G C	G C G T G C	G C T T G C
	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	G C G T C C G	G G G T C G	13 G C G T G C	14 G C G T G C	15 G C G T G C	16 G C G T G C	G C G T G C	G C G T G C	G C G T G C	G C T T G C
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	G C G C C	12 G C G T C G C	13 G C G T G C G	14 G C G T G C G	15 G C G T G C G	16 G C G T G C	G G T G C G	G G T G C G	G G T G C G	G C T T G C G
	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	11 G C G T C C G C	G C G C C T	13 G C G T G C G A	14 G C G T G C G A C	G C G C G A C	16 G C G T G C G	G C G C C	G G T G C G C	G G T G C G C	G C T T G C G C
	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	G C C C C T	12 G C G T C C G C T	G G G T G C G A C	14 G C G T G C G A C	G G T G C G A C	16 G C G T G C C C	G C G T G C G C	G C G T G C G C	G C G T G C G C T	G C T T G C G C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	G C C C C T T	G C G C C C T C T	G C G C G A C T C	14 G C G T G C G A C T T	G C G C G A C T T	16 G C G T G C G C C C	G C G T G C C C T T	G C G T G C G C T T	G C G T G C C C T T	G C T T G C G C T T
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	G C C C C T T C	G C G T C C G C T C C T C	G C G T C C C	14 G C G T G C G A C T T C	G C G C C T C C	16 G C G T G C C T C C	G C G T G C C T T C	G C G T G C G C T T C	G C G T G C G C C T T C	G C T T G C G C C T T
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	G C C C C T T C G	G C G C T C C G C T C G	G C G C C C A	14 G C G T G C G A C T T C G	G C G C C T C C G	16 G C G T G C C T C C G	G C G T G C C C T T C A	G C G T G C G C C T T C G	G C G T G C G C C T T C G	G C T T G C G C C T T C G
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	11 G C G T C C G C C T T C G C	G C C C C C C C C C C C C C C C C C C C	G C G C C C A C	14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C	16 G C G T G C C C C G C	G C G C C T T C A C	G C G T G C G C T T C G C	G C G T G C G C T T C G C	G C T T G C C C T T C G C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	11 G C G T C C G C C T T C G C A	12 G C G T C C G C T C G C A	13 G C G T G C G A C T C C A C A	14 G C G T G C G A C T T C G C A	15 G C G T G C G A C T T C G C A	16 G C G T G C C T C C G C A	G C G T G C C T T C A C A	G C G T G C G C C T T C G C A	G C G T G C G C T T C G C A	G C T T G C C C T T C G C A
40 45	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	11 G C G T C C G C C T T C G C A A	12 G C G T C C G C T C G C A G	13 G C G T G C G A C T C C A C A A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	16 G C G T C C C C C A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	G C G T G C G C C T T C G C A A	G C G T G C G C T T C G C A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
40 45	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	11 G C G T C C G C C T T C G C A A A	12 G C G T C C G C T C T C G C A G C	13 G C G T G C G A C T C C A C A A A	14 G C G T G C G A C T T C G C A A A	15 G C G T G C G A C T T C G C A A A	16 G C G T G C C T C C G C A A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	G C G T G C G C C T T C G C A A A	G C G T G C G C C T T C G C A A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
40 45	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459 10203	11 G C G T C C G C C T T C G C A A A A	12 G C G T C C G C T C T C G C A G C G	13 G C G T G C G A C T C C A C A A A G	14 G C G T G C G A C T T C G C A A A G	15 G C G T G C G A C T T C G C A A A G	16 G C G T G C C T C C G C A A A G	G C G T G C G C C T T C A C A A A G	G C G T G C G C C T T C G C A A A G	G C G T G C G C C T T C G C A A A G	G C T T G C G C C T T C G C A A A G
40 45	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	11 G C G T C C G C C T T C G C A A A	12 G C G T C C G C T C T C G C A G C	13 G C G T G C G A C T C C A C A A A	14 G C G T G C G A C T T C G C A A A	15 G C G T G C G A C T T C G C A A A	16 G C G T G C C T C C G C A A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	G C G T G C G C C T T C G C A A A	G C G T G C G C C T T C G C A A A	G C T T G C G C C T T C G C A A A

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	PS	PS	Haj	plotyp	e Number(c) (Part 3)
	No.(a)	Position(b)	21	22	
	1	504	G	T	
60	2	717	$\mathbf{T}$	C	
	3	744	G	G	
	4	778	C	T	
	5	1009	C	G	
	6	1045	Ç G	C	
65	7	1122		G	
	8	1218	C	С	
	9	2014	С	C	
	10	2177	T	T	
•	11	5906	$\boldsymbol{C}$	T	
70	12	6010	C	C	
	13	8110	G	Α	
	14	8333	С	C	
	15	8354	Α	Α	•
	16	8402	Α	Α	
75	17	8459	Α	Α	
	18	10203	G	G	
	19	10512	T	C	

- (a) PS = polymorphic site;
- (b) Position of PS within SEQ ID NO:1;
  - (c) Alleles for haplotypes are presented 5' to 3' in each column;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions in SEQ ID NO:1 and identities are set forth in the table immediately below:

	PS	PS	Hap	lotype F	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
90	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
95	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
	11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
100	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	، 8110	G/G	G/G	G/G	G/G	G/G	G/G-	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
,	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
105	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T,	T/T	T/T	T/T	T/T	T/T	T/T

	PS	PS	Hap	lotype P	air(c) (P	art 2)				
110	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G							
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G							
	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
115	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	7	1122	G/G							
	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
*	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
120	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C							
125	15	8354	A/A							
	16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
	19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
130										
	PS	PS		olotype I				10100	40/=	10/10
	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
	1	504	G/G							
	2	717	C/C							
135	3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
	4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
	5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G C/C
	6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	G/G
٠	7	1122	G/G	G/G	G/A	G/G	G/A	G/G C/C	G/G C/C	C/C
140	8	1218	C/C	C/C	C/C	C/A	A/C C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C T/T	T/T	T/T	T/C	T/T
	10	2177	T/T							
	11	5906	C/T	T/C	T/T	1/1 C/C	C/C	C/C	C/T	C/C
1.45	12	6010	C/C	C/C G/G	C/C G/G	G/G	G/G	G/G	G/G	G/G
145	13	8110	G/G	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	14	8333	C/C A/A	A/A						
	15	8354	A/A A/A	A/A A/A	A/A A/A	A/A	A/A	A/A	A/G	A/A
	16	8402	A/A A/A	A/A A/A	A/A A/A	A/A A/A	A/A A/A	A/A A/A	A/A	A/A
150	17	8459 10 <b>2</b> 03	G/G							
150	18 19	10203	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C
	19	10312	1/1	1/1	1/0	I/ I	1/0	1/1	1/1	2,0

	PS	PS	Hap	lotype P	air(c) (P	art 4)				
	No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
155	1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
160	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
100	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
165	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
170	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T
175	PS	PS	Haı	olotype l	Pair(c) (	Part 5)				,
175	PS	PS Position(b)		olotype	Pair(c) (	Part 5)				•
175	No.(a)	Position(b)	3/14	olotype l	Pair(c) (	Part 5)				
175	No.(a)	Position(b) 504	3/14 G/G	olotype l	Pair(c) (	Part 5)				•
175	No.(a) 1 2	Position(b) 504 717	3/14 G/G C/C	olotype l	Pair(c) (	Part 5)				•
	No.(a) 1 2 3	Position(b) 504 717 744	3/14 G/G C/C G/G	plotype l	Pair(c) (	Part 5)				•
175 180	No.(a) 1 2 3 4	Position(b) 504 717 744 778	3/14 G/G C/C	olotype l	Pair(c) (	Part 5)				•
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	3/14 G/G C/C G/G C/T	olotype l	Pair(c) (	Part 5)				•
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778	3/14 G/G C/C G/G C/T G/G	olotype l	Pair(c) (	Part 5)				
	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045	3/14 G/G C/C G/G C/T G/G T/C	olotype l	Pair(c) (	Part 5)				•
180	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122	3/14 G/G C/C G/G C/T G/G T/C A/G	olotype l	Pair(c) (	Part 5)				
	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122 1218	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	plotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	olotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C	olotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G	plotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C	olotype I	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A	plotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	olotype l	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	olotype I	Pair(c) (	Part 5)				
180	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	plotype I	Pair(c) (	Part 5)				

<sup>(</sup>a) PS = polymorphic site;

(b) Position of PS in SEQ ID NO:1;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF11B 12. or to a drug for treating a condition or disease predicted to be associated with TNFRSF11B

<sup>(</sup>c) Haplotype pairs are represented as 1<sup>st</sup> haplotype/2<sup>nd</sup> haplotype; with alleles of each haplotype shown 5' to 3' as 1<sup>st</sup> polymorphism/2<sup>nd</sup> polymorphism in each column;

activity.

- 13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF11B gene at a region containing the polymorphic site.
- 15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-21, the complements of SEQ ID NOS:4-21, and SEO ID NOS:22-57.
- 16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.
- 17. The primer-extension oligonucleotide of claim 16, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:58-93.
- 18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 19. The kit of claim 18, which further comprises oligonucleotides designed to genotype or haplotype PS5, wherein the selected PS has the position and alternative alleles shown in SEQ ID NO:1.
- 20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the TNFRSF11B isogene is selected from the group consisting of isogenes 1- 18 and 20 22 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1- 18 and 20 22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Region	PS	PS	Iso	gene N	lumber	r(d) (P	art 1)					
Examined(a)	No.(b)	Position(c)	1	.2	3	4	5	6	7	8	9	10
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	G
427-1437	4	778	C	C	C	C	C	C	C	T	T	T
427-1437	5	1009	С	С	G	G	G	G	G	C	C	C
427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
427-1437	7	1122	G	G	Α	G	G	G	G	G	G	G
427-1437	8	1218	C	C	C	C	C	С	C	A	Α	C
1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
5748-6485	11	5906	C	T	T	C	T	T	T	C	T	C
5748-6485	12	6010	C	C	C	C	C	T	Т	C	C	C
8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
8035-8653	14	8333	C	C	C	C	Ċ	C	T	C	C	C
8035-8653	15	8354	Α	A	$\mathbf{A}$	Α	A	Α	Α	G	A	Α
8035-8653	16	8402	A	Α	Α	A	Α	A	G	A.	Α	Α
8035-8653	17	8459	Α	Α	Α	Α	Α	Α	Α	A	Α	Α
9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
9942-10628	19	10512	Т	T	С	T	T	T	T	Т	T	T
Region	PS	PS				r(d) (P	-					
Examined(a)	No.(b)	Position(c)	11	12	13	14	15	16	17	18	20	
Examined(a) 427-1437	No.(b)	Position(c) 504	11 G	12 G	13 G	14 G	15 G	G	G	G	G	
Examined(a) 427-1437 427-1437	No.(b) 1 2	Position(c) 504 717	11 G C	12 G C	13 G C	14 G C	15 G C	G C	G C	G C	G C	
Examined(a) 427-1437 427-1437 427-1437	No.(b) 1 2 3	Position(c) 504 717 744	11 G C G	12 G C G	13 G C G	14 G C G	15 G C G	G C G	G C G	G C G	G C T	
Examined(a) 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4	Position(c) 504 717 744 778	11 G C G T	12 G C G T	13 G C G T	14 G C G T	15 G C G T	G C G T	G C G T	G C G T	G C T T	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5	Position(c) 504 717 744 778 1009	G C G T C	12 G C G T	13 G C G T G	14 G C G T	15 G C G T G	G C G T G	G C G T G	G C G T G	G C T T G	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6	Position(c) 504 717 744 778 1009 1045	G C G T C C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	G C G T G C	G C G T G C	G C G T G C	G C T T G C	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6 7	Position(c) 504 717 744 778 1009 1045 1122	11 G C G T C C	12 G C G T C C G	13 G C G T G C	14 G C G T G C	15 G C G T G C	G C G T G C G	G C G T G C G	G G T G C G	G C T G C	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6 7 8	Position(c) 504 717 744 778 1009 1045 1122 1218	II G C G T C C G	12 G C G T C G C	13 G C G T G C G	14 G C G T G C G	15 G C G T G C G	G C G T G C G C	G C G C C	G C G C C	G C T T G C G	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208	No.(b) 1 2 3 4 5 6 7 8 9	Position(c) 504 717 744 778 1009 1045 1122 1218 2014	II G C G T C C G C	12 G C G T C C G	G C G T G C G A C	14 G C G T G C G A	15 G C G T G C G A	G C G T G C G C C	G C G C C C	G G T G C G C	G C T T G C G C	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208	No.(b)  1  2  3  4  5  6  7  8  9 10	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177	G C C C C C T	12 G C G T C G C T	G C G C G A C T	14 G C G T G C G A C	15 G C G T G C G A C	G C G C C T	G C G T G C G C C	G G T G C G C	G C T T G C G C T	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485	No.(b)  1  2  3  4  5  6  7  8  9  10  11	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	II G C G T C C G C C T T	12 G C G T C C G C T	13 G C G T G C G A C T	14 G C G T G C G A C T	15 G C G T G C G A C T	G C G C C T C	G C G T G C C T T	G C G T G C G C T T	G C T T G C G C T T	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	G C C C C C T T C	12 G C G T C C G C T C T C	13 G C G T G C G A C T C C	G C G A C T T C	15 G C G T G C G A C T T	G C G C C C C C C C C C C C C C C C C C	G C G C G C C T T C	G C G C C T T C	G C T G C G C T T	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	G C C C C C T T C G	12 G C G T C C G C T C T C G	13 G C G T G C G A C T C C A	14 G C G T G C G A C T T C G	15 G C G T G C G A C T T C G	GCGTGCGCCTCCG	G C G C C T T C A	G C G T G C C T T C G	G C T T G C G C T T C G	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13  14	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	G C C C C T T C C C C C	12 G C G T C C G C T C G C	13 G C G T G C G A C T C C A C	14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C	GCGTGCGCTCCGC	G C G C C T T C A C	G C G C C T T C G C	G C T T G C G C T T C G C	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13  14  15	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	G C C C C C T T C C C A	12 G C G T C C G C T C G C A	13 G C G T G C G A C C A C A	14 G C G T G C G A C T T C G C A	15 G C G T G C G A C T T C G C A	G C G T G C G C C T C C G C A	G C G C C T T C A C A	G C G C C T T C G C A	G C T T G C C T T C G C A	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	11 G C G T C C G C C T T C G C A A	12 G C G T C C G C T C G C A G	13 G C G T G C G A C T C C A A C	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	G C G T G C G C C T C C G C A A	G C G C C T T C A C A A	G C G C C T T C G C A A	G C T T G C G C C T T C G C A A	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16  17	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	11 G C G T C C G C C T T C G C A A A	12 G C G T C C G C T C T C G C A G C	13 G C G T G C G A C T C C A A A A	14 G C G T G C G A C T T C G C A A A	15 G C G T G C G A C T T C G C A A A	G C G T G C G C C T C C G C A A A	G C G C C T T C A C A A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	G C T T G C C T T C G C A A A	
Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	No.(b)  1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	11 G C G T C C G C C T T C G C A A	12 G C G T C C G C T C G C A G	13 G C G T G C G A C T C C A A C	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	G C G T G C G C C T C C G C A A	G C G C C T T C A C A A	G C G C C T T C G C A A	G C T T G C G C C T T C G C A A	

Region	PS	PS	Iso	gene l	Number(d) (Part 3)
Examined(a)	No.(b)	Position(c)	21	22	
427-1437	1	504	G	T	
427-1437	2	717	T	C	
427-1437	3	744	G	G	
427-1437	4	778	C	T	
427-1437	5	1009	C	G	
427-1437	6	1045	· C	C	
427-1437	7	1122	G	G	
427-1437	8	1218	C	C	
1604-2208	9	2014	C	C	
1604-2208	10	2177	T	$\mathbf{T}_{i}$	
5748-6485	11	5906	C	T'	
5748-6485	12	6010	C	C	
8035-8653	13	8110	G	Α	
8035-8653	14	8333	C	C	
8035-8653	15	8354	Α	Α	
8035-8653	16	8402	Α	Α	
8035-8653	17	8459	Α	A	
9942-10628	18	10203	G	G	
9942-10628	19	10512	T	C	

- (a) Region examined represents the nucleotide positions defining the start and stop positions within the 1<sup>st</sup> SEQ ID NO of the sequenced region;
- (b) PS = polymorphic site;
- (c) Position of PS in SEQ ID NO:1;
- (d) Alleles for isogenes are presented 5' to 3' in each column;
- (b) a second nucleotide sequence which is complementary to the first nucleotide sequence.
- 21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.
- 22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 21, wherein the organism expresses a TNFRSF11B protein that is encoded by the first nucleotide sequence.
- 23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.
- 24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, thymine at PS2, thymine at PS3, cytosine at PS4, thymine at PS6, adenine at PS7, adenine at PS8, thymine at PS9, cytosine at PS10, cytosine at PS11, thymine at PS12, adenine at PS13, thymine at PS14, guanine at PS15, guanine at PS16, cytosine at PS17, adenine at PS18 and cytosine at PS19, wherein the selected polymorphism has the position set forth in the table immediately below:

10								43					
	Region	PS	PS	Isog		umber(		rt 1)	_	7	8	9	10
	Examined(a)	No.(b)	Position(c)	1	. 2	3	4	5	6	7	Ğ	G	G
	427-1437	1	504	G	G	G	G	G	G	G		C	C
	427-1437	2	717	C	C	C	C	C	C	C	C		G
15	427-1437	3	744	G	G	G	G	G	G	G	G	G	T
	427-1437	4	778	C	C	C	C	C	C	C	T	T	
	427-1437	5	1009	C	C	G	G	G	G	G	C	C	C
	427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
	427-1437	7	1122	G	G	A	G	G	G	G	G	G	G
20	427-1437	8	1218	C	C	C	C	C	C	C	A	A	C
	1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
	1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
	5748-6485	11	5906	C	T	T	C	T	T	T	C	T	C
	5748-6485	12	6010	C	C	C	C	C	T	T	C	C	C
25	8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
	8035-8653	14	8333	C	C	C	C	C	C	T.	C	C	C
	8035-8653	15	8354	Α	Α	Α	Α	Α	Α	A	G	A	A
	8035-8653	16	8402	Α	Α	Α	Α	Α	Α	G	A	A	A
	8035-8653	17	8459	Α	Α	Α	Α	A	A	A	A	A	A
30	9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
	9942-10628	19	10512	T	T	C	T	T	T	T	T	T	T
	Region	PS.	PS			Jumbe	r(d) (P	art 2)	1.0	17	10	20	
	Examined(a)	No.(b)	Position(c)	11	12	13	14	15	16	17	18 G	G	
35	427-1437	1	504	G	G	G	G	G	G	G	C	C	
	427-1437	2	717	,C	C	C	C	C	C	C G	G	T	
	427-1437	3	744	G	G	G	G	G	G		T	T	
	427-1437	4	778	T	T	T	T	T	T	T G	G G	G	
	427-1437	5	1009	C	C	G	G	G	G	C	C	C	
40	427-1437	6	1045	C	C	C	C	C	C	G	G	G	
	427-1437	7	1122	G	G	G	G	G	G	C	C	C	
	427-1437	8	1218	C	C	A	A	A	C	C	C	Č	
	1604-2208	9	2014	C	T	C	C	C	C	T	T	T	
	1604-2208	10	2177	T	C	T	T	T	T	T	T	Ť	
45	5748-6485	11	5906	T	T	C	T ·	T	C	C	C	Ċ	
	5748-6485	12	6010	C	C	C	C	C	C		G	G	
	8035-8653	13	8110	G	G	A	G	G	G	A	_	C	
	8035-8653	14	8333	C	C	C	C	C	C	C	C	A	
	8035-8653	15	8354	A	A	A	A	A	A	A	A	A	*
50	8035-8653	16	8402	Α	G	A	A	A	A	A	A	A	
	8035-8653	17	8459	Α	C	A	A	A	A	A	A	G	
	9942-10628		10203	A	G	G	G	G	G	G	G C	T	
	9942-10628	19	10512	T	T	C	C	T	Т	T	C	1	

55	Region	PS	PS	Iso	gene N	Number(d) (Part 3)
	Examined(a)	No.(b)	Position(c)	21	22	
_	427-1437	1	504	G	T	
	427-1437	2	717	T	C	
	427-1437	3	744	G	G	
60	427-1437	4	778	C	T	
	427-1437	5	1009	C	G	
	427-1437	6	1045	C	C	
	427-1437	7	1122	G	G	
	427-1437	8	1218	C	C	
65	1604-2208	9	2014	C	C	
	1604-2208	10	2177	T	Τ	
	5748-6485	11	5906	C	T	
	5748-6485	12	6010	C	C	_
	8035-8653	13	8110	G	Α	
70	8035-8653	14	8333	C	C	
	8035-8653	15	8354	Α	Α	
	8035-8653	16	8402	Α	Α	
	8035-8653	17	8459	Α	Α	
	9942-10628	18	10203	G	G	
75	9942-10628	19	10512	T	C	

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;

(b) PS = polymorphic site;

(c) Position of PS within SEQ ID NO:1;

(d) Alleles for TNFRSF11B isogenes are presented 5' to 3' in each column.

25. An isolated polynucleotide comprising a coding sequence for a TNFRSF11B isogene, wherein the coding sequence comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

PS	PS	Isoge	ene Codi	ng Sec	quence	Numb	er(c)	(Part 1	)		
No.(a)	Position(b)	1c	2c	3c	7c	8c	9c	10c	11c	12c	13c
5	9 `´	C	С	G	G	C	C	С	C	C	G
14	699	С	C	C	T	C	C	C	C	C	C
- 15	720	Α	Α	Α	Α	G	Α	Ά	Α	Α	Α
16	768	Α	A	Α	G	Α	Α	Α	Α	G	Α
18	841	G	G	G	G	G	G	G	Α	G	G
19	1150	T	T	C	T	T	T	T	T	Т	С
PS	PS	Isog	ene Codi	ing Se	quence	Numl	ber(c)	(Part 2	)		
No.(a)	Position(b)	14c	18c	21c	22c						
- 5	9 `´	G	G	C	G						
14	699	C	C	C	C						
15	720	Α	Α	Α	Α						
16	768	Α	Α	Α	Α						
18	841	G	G	G	G						
19	1150	C	C	T	C						

<sup>(</sup>a) PS = polymorphic site;

(b) Position of PS in SEQ ID NO:2;

<sup>(</sup>c) Alleles for the isogene coding sequence are presented 5' to 3' in each column; the numerical

- portion of the isogene coding sequence number represents the number of the parent full TNFRSF11B isogene.
- 26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein that is encoded by the polymorphic variant sequence.
- 27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.
- 28. An isolated fragment of a TNFRSF11B coding sequence, wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at a position corresponding to nucleotide 699, guanine at a position corresponding to nucleotide 720, guanine at a position corresponding to nucleotide 841 and cytosine at a position corresponding to nucleotide 1150 in SEQ ID NO:2.
- An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281.
- 30. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.
- 31. A method for screening for drugs targeting the isolated polypeptide of claim 29 which comprises contacting the TNFRSF11B polymorphic variant with a candidate agent and assaying for binding activity.
- 32. An isolated fragment of a TNFRSF11B protein, wherein the fragment comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281 in SEQ ID NO:3.
- 33. A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) gene, comprising:
  - (a) a central processing unit (CPU);
  - (b) a communication interface;
  - (c) a display device;

- (d) an input device; and
- (e) a database containing the polymorphism data; wherein the polymorphism data comprises the haplotypes set forth in the table immediately below:

10	PS No.(a)	PS Position(b)	Ha <sub>l</sub> 1	plotypo	e Num 3	ber(c) 4	(Part 1	.) 6	7	8	9	10
	1	504	Ġ	Ğ	G	Ğ	G	Ğ	Ğ	Ğ	G	G
	2	717	Č	Č	Č	Č	Č	Č	Č	Č	Č	Č
	3	744	G	G	G	G	G	G	G	G	G	G
15	4	778	C	C	C	C	C	C	C	T	T	T
	5	1009	C	C	G	G	G	G	G	C	$\boldsymbol{C}$	C
	, 6	1045	C	C	Τ	T	T	T	T	C	C	C
-	, <u>7</u>	1122	G	G	A	G	G	G	G	G	G	G
	8	1218	C	C	C	C	C	C	C	A	A	C
20	9	2014	C	C	C	C	C	C	T	C	C	C
	10	2177	T	T	T	T	T	T	C	T	T	T C
	11 12	5906	C C	T C	T C	C C	T C	T T	T T	C C	T C	C
	13	6010 8110	G	G	G	G	G	G	Ğ	G	G	G
25	13	8333	C	C	C	C	C	C	T	C	C	Č
23	15	8354	A	A	A	Ā	A	Ä	Â	Ğ	Ā	Ã
	16	8402	Ā	A	A	A	A	A	G	Ā	A	A
	17	8459	A	Α	A	A	A	Α	Α	A	Α	Α
	18	10203	G	G	G	G	G	G	G	G	G	G
30	19	10512	T	T	C	T	T	T	T	T	T	T
	DC	DC	Ца	nlotem	a Num	hor(a)	(Dort	) \ 				
	PS	PS Position(b)				ber(c)			17	18	19	20
	No.(a)	Position(b)	11	12	13	14	15	16	17 G	18 G	19 G	20 G
35	No.(a) 1	Position(b) 504	11 G	12 G	13 G	14 G	15 G	16 G	G	G	G	G
35	No.(a)	Position(b)	11	12	13	14	15	16				
35	No.(a) 1 2 3 4	Position(b) 504 717	11 G C	12 G C	13 G C	14 G C	15 G C	16 G C	G C	G C	G C	G C T T
35	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	II G C G T C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G	G C G T G	G C G T G	G C T T G
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	II G C G T C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G C	G C G T G C	G C G T G C	G C T G C
35 40	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	II G C G T C C	12 G C G T C C G	13 G C G T G C	14 G C G T G C	15 G C G T G C	16 G C G T G C	G C G T G C	G G G T G C G	G C G T G C G	G C T G C
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	11 G C G T C C G	12 G C G T C C G	13 G C G T G C G	14 G C G T G C G	15 G C G T G C G	16 G C G T G C G	G C G T G C G	G C G T G C G C	G G G T G C G	G C T G C G
	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	G C C C C	12 G C G T C C G C	13 G C G T G C G A	14 G C G T G C G A	15 G C G T G C G A	16 G C G T G C G C	G G T G C G C	G C G T G C G C C	G C G T G C G C	G C T G C G C
	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	11 G C G T C C G C C	12 G C G T C G C T C	13 G C G T G C G A C	14 G C G T G C G A C	15 G C G T G C G A C	16 G C G T G C G C C T	G C G T G C G C	G C G T G C G C C T	G C G T G C G C C	G C T G C G C C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	G C C C T T	12 G C G T C C G C T C	13 G C G T G C G T	14 G C G T G C G A C T	15 G C G T G C G A C T	16 G C G T G C G C C C	G C G T G C G C T T	G C G C C T T	G C G C C C T T	G C T T G C G C T T
	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	G C C C C T T C	12 G C G T C C G C T C T C T C	13 G C G T G C G A C T C C	G C G C G A C T T C	15 G C G T G C G A C T T	16 G C G T G C G C C T C	G C G C G C C T T C	G C G C C T T C	G C G C C C T T C	G C T G C G C C T T C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	G C C C C T T C G	12 G C G T C C G C T C G G	G C G A C T C C A	G C G C C T T C G	G C G C G A C T T C G	16 G C G T G C C T C C G	G C G C G C C T T C A	G C G T G C G C C T T C G	G C G T G C C T T C G	G C T T G C G C T T C G
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	G C C C T T C G C	12 G C G T C C G C T C G C	G C G A C T C C A C	G C G A C T T C G C	G C G A C T T C G C	16 G C G T G C C C C C C C	G C G C C C C T C A C	G C G T G C G C C T T C G C	G C G T G C C T T C G C	G C T T G C G C T T C G C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	G C C C C T T C G	12 G C G T C C G C T C G G	G C G A C T C C A	G C G C C T T C G	G C G C G A C T T C G	16 G C G T G C C T C C G	G C G C G C C T T C A	G C G T G C G C C T T C G	G C G T G C C T T C G	G C T T G C G C T T C G
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	G C C C C T T C G C A	12 G C G T C C G C T C G C A	G C G A C C A C A	14 G C G T G C G A C T T C G C A	G C G C C C C A	16 G C G C C C C C C C A	G C G C C T T C A C A	G C G T G C G C C T T C G C A A A	G G G C G C C T T C G C A	G C T T G C G C A A A
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	G C C C C T C C C A A	12 G C G T C C G C T C G C A G	G C G C C C A C C A A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	16 G C G C C C C C C A A	G C G C C T T C A C A A	G C G T G C G C T T C G C A A	G C G C C T T C G C A A	G C T T G C G C A A

	PS	PS	Hap	lotyr	e Number(c) (Part 3)
55	No.(a)	Position(b)	21	22	
	1	504	G	T	
	2	717	T	C	
	3	744	G	G	
	4	778	C	T	
60	5	1009	C	G	
	6	1045	C	C	
	7	1122	G	G	
	8	1218	C	C	
	9	2014	C	C	
65	10	2177	T	T	
	11	5906	С	T	
	12	6010	C	C	
	13	8110	G	Α	
	14	8333	С	C	
70	15	8354	Α	Α	
	16	8402	Α	Α	
	17	8459	Α	Α	
	18	10203	G	G	
	19	10512	T	C	•
75					

- (a) PS = polymorphic site;
  (b) Position of PS within SEQ ID NO:1;
  (c) Alleles for haplotypes are presented 5' to 3' in each column;

the haplotype pairs set forth in the table immediately below: 80

	PS	PS	Hap	lotype P	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
85	2 .	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
90	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
	11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
95	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
100	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	- 10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

	PS	PS	Hap	lotype P	air(c) (F	art 2)				
105	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
110	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	7	1122	G/G	G/G ,		G/G	G/G	G/G	G/G	G/G
	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
115	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
100	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C A/A	C/C A/A
120	15	8354	A/A	A/A	A/A	A/A A/G	A/A A/A	A/A A/A	A/A A/A	A/A A/A
	16 17	8402 8459	A/A A/A	A/A A/A	A/A A/A	A/G A/C	A/A A/A	A/A A/A	A/A A/A	A/A A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
	19	10203	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
125	19	10312	1/0	1/0	170	1/1	1/1		1/1	1/1
123	PS	PS	Har	lotype P	Pair(c) (F	Part 3)				
	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~								
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		504 717	G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C
130	1 2 3	-								
130	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
130	2 3 4 5	717 744 778 1009	C/C G/G C/C C/C	C/C G/G T/C G/G	C/C G/G T/C G/G	C/C G/G T/T G/C	C/C G/G T/C G/G	C/C G/T T/T G/G	C/C G/G T/C G/G	C/C G/G T/T G/G
130	2 3 4 5 6	717 744 778 1009 1045	C/C G/G C/C C/C C/C	C/C G/G T/C G/G C/T	C/C G/G T/C G/G C/T	C/C G/G T/T G/C C/C	C/C G/G T/C G/G C/T	C/C G/T T/T G/G C/C	C/C G/G T/C G/G C/T	C/C G/G T/T G/G C/C
	2 3 4 5 6 7	717 744 778 1009 1045 1122	C/C G/G C/C C/C C/C G/G	C/C G/G T/C G/G C/T G/G	C/C G/G T/C G/G C/T G/A	C/C G/G T/T G/C C/C G/G	C/C G/G T/C G/G C/T G/A	C/C G/T T/T G/G C/C G/G	C/C G/G T/C G/G C/T G/G	C/C G/G T/T G/G C/C G/G
130 135	2 3 4 5 6 7 8	717 744 778 1009 1045 1122 1218	C/C G/G C/C C/C C/C G/G C/C	C/C G/G T/C G/G C/T G/G C/C	C/C G/G T/C G/G C/T G/A C/C	C/C G/G T/T G/C C/C G/G C/A	C/C G/G T/C G/G C/T G/A A/C	C/C G/T T/T G/G C/C G/G C/C	C/C G/G T/C G/G C/T G/G C/C	C/C G/G T/T G/G C/C G/G C/C
	2 3 4 5 6 7 8 9	717 744 778 1009 1045 1122 1218 2014	C/C G/G C/C C/C C/C G/G C/C	C/C G/G T/C G/G C/T G/G C/C C/C	C/C G/G T/C G/G C/T G/A C/C C/C	C/C G/G T/T G/C C/C G/G C/A C/C	C/C G/G T/C G/G C/T G/A A/C C/C	C/C G/T T/T G/G C/C G/G C/C	C/C G/G T/C G/G C/T G/G C/C C/T	C/C G/G T/T G/G C/C G/G C/C
	2 3 4 5 6 7 8 9	717 744 778 1009 1045 1122 1218 2014 2177	C/C G/G C/C C/C C/C G/G C/C C/C	C/C G/G T/C G/G C/T G/G C/C C/C	C/C G/G T/C G/G C/T G/A C/C C/C T/T	C/C G/G T/T G/C C/C G/G C/A C/C T/T	C/C G/G T/C G/G C/T G/A A/C C/C T/T	C/C G/T T/T G/G C/C G/G C/C C/C T/T	C/C G/G T/C G/G C/T G/G C/C C/T T/C	C/C G/G T/T G/G C/C G/G C/C C/C T/T
	2 3 4 5 6 7 8 9 10 11	717 744 778 1009 1045 1122 1218 2014 2177 5906	C/C G/G C/C C/C G/G C/C C/C T/T C/T	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T	C/C G/G T/T G/C C/C G/G C/A C/C T/T	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T	C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T
135	2 3 4 5 6 7 8 9 10 11 12	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	C/C G/G C/C C/C G/G C/C C/C T/T C/T C/C	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T	C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T C/C
	2 3 4 5 6 7 8 9 10 11 12 13	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	C/C G/G C/C C/C G/G C/C C/C T/T C/T C/C G/G	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G	C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G
135	2 3 4 5 6 7 8 9 10 11 12 13 14	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	C/C G/G C/C C/C G/G C/C C/C C/C C/C C/C	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G C/C	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G C/T	C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
135	2 3 4 5 6 7 8 9 10 11 12 13 14 15	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	C/C G/G C/C C/C G/G C/C C/C T/T C/T C/C G/G C/C A/A	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G C/C A/A	C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A	C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A
135	2 3 4 5 6 7 8 9. 10 11 12 13 14 15 16	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	C/C G/G C/C C/C G/G C/C T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G C/T A/A A/G	C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
135	2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	C/C G/G C/C C/C G/G C/C C/C T/T C/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G C/T A/A A/G A/A	C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
135	2 3 4 5 6 7 8 9. 10 11 12 13 14 15 16	717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	C/C G/G C/C C/C G/G C/C T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C G/G C/C A/A A/A	C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G C/T A/A A/G	C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A

	PS	PS	Han	lotype P	air(c) (F	art 4)				
	No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
150	1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
•	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
160	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
165	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4.0	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T
	19	10312	C/ 1	1/1	1/1					
170							, ,	-/ -	-/-	
	PS	PS	Hap	lotype P				<b>2</b> / 2	- · -	
	PS No.(a)		Hap 3/14					-/-	<u>-</u>	
* *	PS No.(a)	PS Position(b) 504	Hap 3/14 G/G					-/-		
* *	PS No.(a)	PS Position(b)	Hap 3/14					-7-		
* *	PS No.(a) 1 2	PS Position(b) 504 717	Hap 3/14 G/G C/C				.717			
	PS No.(a) 1 2 3 4	PS Position(b) 504 717 744	Hap 3/14 G/G C/C G/G							
	PS No.(a) 1 2 3	PS Position(b) 504 717 744 778	Hap 3/14 G/G C/C G/G C/T				.7.7			
	PS No.(a) 1 2 3 4 5	PS Position(b) 504 717 744 778 1009	Hap 3/14 G/G C/C G/G C/T G/G				.717			
	PS No.(a) 1 2 3 4 5 6	PS Position(b) 504 717 744 778 1009 1045	Hap 3/14 G/G C/C G/G C/T G/G T/C				.717			
	PS No.(a) 1 2 3 4 5 6 7	PS Position(b) 504 717 744 778 1009 1045 1122	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G							
175	PS No.(a) 1 2 3 4 5 6 7 8	PS Position(b) 504 717 744 778 1009 1045 1122 1218	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A							
175	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A							

or the frequency data in Tables 6 and 7.

A genome anthology for the tumor necrosis factor receptor superfamily, member 11b 34. (osteoprotegerin) (TNFRSF11B) gene which comprises two or more TNFRSF11B isogenes

<sup>(</sup>a) PS = polymorphic site;(b) Position of PS in SEQ ID NO:1;

<sup>(</sup>c) Haplotype pairs are represented as 1<sup>st</sup> haplotype/2<sup>nd</sup> haplotype; with alleles of each haplotype shown 5' to 3' as 1<sup>st</sup> polymorphism/2<sup>nd</sup> polymorphism in each column;

selected from the group consisting of isogenes 1-22 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	Region	PS	PS	Isog	gene N	umber	(d) (Pa	rt 1)	1				
10	Examined(a)	No.(b)	Position(c)	1	2	3	4	5	6	7	8	9	10
	427-1437	1	504	G	G	G	G	G	G	G	G	G	G
	427-1437	. 2	717	C	C	C	C	C	C	C	C	C	C
	427-1437	3	744	G	G	G	G	G	G	G	G	G	G
	427-1437	4	778	C	C	C	C	C	C	C	T	T	T
15	427-1437	5	1009	C	C	G	G	G	G	G	C	C	C
	427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
	427-1437	7	1122	G	G	Α	G	G	G	G	G	G	G
	427-1437	8	1218	C	C	C	C	C	C	C	Α	A	C
	1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
20	1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
	5748-6485	11	5906	C	T	T	C	Ť	T	T	C	T	C
*	5748-6485	12	6010	C	C	C	C	C	T	T	C	C	C
	8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
	8035-8653	14	8333	C	C	C	C	C	C	T	C	C	C
25	8035-8653	15	8354	Α	Α	Α	Α	Α	Α	Α	G	A	Α
	8035-8653	16	8402	Α	Α	Α	Α	Α	Α	G	A	Α	Α
	8035-8653	17	8459	Α	Α	Α	Α	Α	Α	Α	A	Α	A
	9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
	9942-10628	19	10512	T	Т	C	T	T	T	T	T	T	T
	9942-10020	17	10012	~									
30	9942-10020												
30	Region	PS	PS	Iso	gene N	Jumbei	r(d) (P	art 2)				. 10	20
30		PS	PS Position(c)	Iso 11	gene N	Jumbei 13	14	15	16	17	18	19	20
30	Region Examined(a) 427-1437	PS No.(b)	PS Position(c) 504	Iso 11 G	gene N 12 G	Tumbei 13 G	14 G	15 G	G	G	G	G	G
30	Region Examined(a) 427-1437 427-1437	PS No.(b) 1 2	PS Position(c) 504 717	Iso 11 G C	ogene N 12 G C	Jumber 13 G C	14 G C	15 G C	G C	G C	G C	G C	G C
30 35	Region Examined(a) 427-1437 427-1437	PS No.(b) 1 2 3	PS Position(c) 504 717 744	Iso 11 G C G	ogene N 12 G C C	Jumber 13 G C C	14 G C G	15 G C G	G C G	G C G	G C G	G C G	G C T
	Region Examined(a) 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4	PS Position(c) 504 717 744 778	Iso 11 G C G T	gene N 12 G C G T	Jumber 13 G C G T	14 G C G T	15 G C G T	G C G T	G C G T	G C G T	G C G T	G C T T
	Region Examined(a) 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5	PS Position(c) 504 717 744 778 1009	Iso 11 G C G T	gene N 12 G C G T C	Jumber 13 G C G T G	14 G C G T G	15 G C G T G	G C G T G	G C G T G	G C G T G	G C G T G	G C T T G
	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5	PS Position(c) 504 717 744 778 1009 1045	Iso 11 G C G T C	egene N 12 G C G T C	Jumber 13 G C G T G	14 G C G T G	15 G C G T G	G C G T G C	G C G T G C	G C G T G C	G C G T G C	G C T G C
35	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5 6 7	PS Position(c) 504 717 744 778 1009 1045 1122	Iso 11 G C G T C C G	gene N 12 G C G T C G C	Jumber 13 G C G T G C	14 G C G T G C	15 G C G T G C	G C G T G C	G C G T G C	G C G T G C	G C G T G C G	G C T G C
	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5 6 7 8	PS Position(c) 504 717 744 778 1009 1045 1122 1218	Iso 11 G C G T C G C C	gene N 12 G C G T C G C C	Iumber 13 G C G T G C G	14 G C G T G C G	15 G C G T G C G	G G T G C G	G G T G C G	G G T G C G	G G G T G C G	G C T G C G
35	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208	PS No.(b) 1 2 3 4 5 6 7 8	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014	Iso 11 G C G T C C C C C	gene N 12 G C G T C G C T	Jumber 13 G C G T G C G A	14 G C G T G C G A	15 G C G T G C G A	G G G T G C G C	G G T G C G C	G C G T G C G C	G C G T G C G C C	G C T T G C G C
35	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208	PS No.(b) 1 2 3 4 5 6 7 8 9	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177	Iso 11 G C G T C C C C T	egene N 12 G C G T C C G C	Jumber 13 G C G T G C G A C	14 G C G T G C G A C	15 G C G T G C G A C	G C G T G C G C C	G C G T G C G C T	G C G T G C G C	G C G T G C G C C	G C T G C G C C
35	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485	PS No.(b) 1 2 3 4 5 6 7 8 9 10	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	Iso 11 G C G T C C G C T T	gene N 12 G C G T C C T C T T	Jumber 13 G C G T G C T C C C C	14 G C G T G C G A C T	15 G C G T G C G A C T	G C G C C T C	G C G T G C C T T	G C G T G C G C T T	G C G T G C G C T T	G C T G C G C T T
35 40	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 5748-6485 5748-6485	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	Iso 11 G C G T C C C T T C	gene N 12 G C G T C C G T C C C T C	Jumber 13 G C G T G C T C C C	14 G C G T G C G A C T T C	15 G C G T G C G A C T T	G C G C C T C C	G C G C C T T C	G G T G C G C T T C	G C G C C T T C	G C T T G C G C T T C
35	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 5748-6485 5748-6485 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	Iso 11 G C G T C C G C T T C G	gene N 12 G C G T C C G T C G C T C G G T C G	Jumber 13 G C G T G C G A C T C	14 G C G T G C G A C T T C G	G C G C C T C C G	G C G T G C G C C T C C G	G C G T G C C T T C A	G C G T G C G C C T T C G	G C G T G C G C C T T C G	G C T T G C G C T T C G
35 40	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	Iso 11 G C G T C C G C T T C G C	gene N 12 G C G T C C G T C C G C T C C C C C C C	Jumber 13 G C G T G C G A C C A C C	14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C	G C G C C T C C G C	G C G C C T T C A C	G C G T G C G C T T C G C	G C G T G C G C C T T C G C	G C T T G C G C T T C G C
35 40	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	Iso 11 G C G T C C G C T T C G C A	gene N 12 G C G T C C G C T C C G A	Jumber 13 G C G T G C G A C T C A	14 G C G T G C G A C T T C G C A	15 G C G T G C G A C T T C G C A	G C G T G C G C C T C C G C A	G C G C C T T C A C A	G C G T G C C T T C G C A	G C G T G C G C C T T C G C A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
35 40	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Iso 11 G C G T C C G C T T C G C A A	gene N 12 G C G T C C G C T C G C A G	Jumber 13 G C G T G C G A C C A C A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	G C G T G C G C A A	G C G T G C C T T C A C A A	G C G T G C C T T C G C A A	G C G T G C G C C T T C G C A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
35 40 45	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	Iso 11 G C G T C C G C C T T C G C A A A	gene N 12 G C G T C C G C T C G C A G C	Jumber 13 G C G T G C A C A A A	14 G C G T G C G A C T T C G C A A A	15 G C G T G C G A C T T C G C A A A	G C G T G C G C C A A A	G C G T G C G C C T T C A C A A A	G C G T G C G C C T T C G C A A A	G C G T G C G C C T T C G C A A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
35 40	Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Iso 11 G C G T C C G C T T C G C A A	gene N 12 G C G T C C G C T C G C A G	Jumber 13 G C G T G C G A C C A C A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	G C G T G C G C A A	G C G T G C C T T C A C A A	G C G T G C C T T C G C A A	G C G T G C G C C T T C G C A A	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

	Region	PS	PS	Iso	gene Number(d) (Part 3)
55	Examined(a)	No.(b)	Position(c)	21	22
	427-1437	` 1	504	G	T
	427-1437	2	717	T	C
	427-1437	3	744	G	G
	427-1437	4	778	C	T
60	427-1437	5	1009	C	G
	427-1437	6	1045	C	C
	427-1437	7	1122	G	G
•	427-1437	8	1218	C	C
	1604-2208	9	2014	C	C
65	1604-2208	10	2177	T	T ·
	5748-6485	11	5906	C	T
	5748-6485	12	6010	C	C
	8035-8653	13	8110	G	A
	8035-8653	14	8333	C	C
70	8035-8653	15	8354	Α	A
	8035-8653	16	8402	Α	A
	8035-8653	17	8459	Α	A
	9942-10628	18	10203	G	G
	9942-10628	19	10512	T	C
75					

<sup>(</sup>a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:1;
(d) Alleles for TNFRSF11B isogenes are presented 5' to 3' in each column.